

[illegible]

## <120> Particles for Gene Therapy

<140> PCT/DE00/00363

<150> DE 199 04 800.2

<160> 19

&lt;170&gt; PatentIn Ver. 2.1

<210> 1

<211> 347

&lt;212&gt; PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:

Fusion protein comprising a LHBs and heterologous binding site  
RGD

 $\langle 400 \rangle$  1

Met Gly Arg Gly Asp Gly Ala Gly Ala Phe Gly Leu Gly Phe Thr Pro  
1 5 10 15

Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu  
20 25 30

Glu Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser  
35 40 45

Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu Arg Asn Thr His Pro  
50 55 60

Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp  
65 70 75 80

Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly  
85 90 95

Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe  
100 105 110

Ser Arg Ile Gly Asp Pro Ala Leu Asn Met Glu Asn Ile Thr Ser Gly  
115 120 125

Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr  
130 135 140

Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu  
145 150 155 160

Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser

Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro Gly  
 165 170 175  
 180 185 190  
 Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu  
 195 200 205  
 Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met  
 210 215 220  
 Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly  
 225 230 235 240  
 Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr Pro  
 245 250 255  
 Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro  
 260 265 270  
 Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu Trp Ala Ser  
 275 280 285  
 Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe  
 290 295 300  
 Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp  
 305 310 315 320  
 Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe Leu Pro Leu  
 325 330 335  
 Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile  
 340 345

<210> 2  
 <211> 215  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence:  
 Fusion protein comprising a HBcAg, a cell-permeability-  
 mediating polypeptide and heterologous binding site RGD

<400> 2

Met Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Thr Val Gln  
 1 5 10 15  
 Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile Asp Pro  
 20 25 30  
 Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser  
 35 40 45  
 Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu  
 50 55 60  
 Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr  
 65 70 75 80  
 Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala  
 85 90 95

Thr Trp Val Gly Val Asn Leu Glu Asp Pro Glu Phe Arg Gly Asp Ala  
 100 105 110  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
 115 120 125  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 130 135 140  
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 145 150 155 160  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 165 170 175  
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
 180 185 190  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser  
 195 200 205  
 Gln Ser Arg Glu Pro Gln Cys  
 210 215

<210> 3  
 <211> 663  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence:  
 DNA coding for a fusion protein comprising a HBcAg, a cell-  
 permeability-mediating polypeptide and heterologous binding  
 site RGD

<400> 3

atgcccatat cgtcaatctt ctcgaggatt ggggaccctg gatccactac tgttcaagcc 60  
 tccaagctgt gccttggtg gctttggggc atggacatcg acccttataa agaatttgga 120  
 gctactgtgg agttactctc gtttttgcc tctgacttct ttccttcagt acgagatctt 180  
 ctagataccg cctcagctct gtatcgggaa gccttagagt ctctgagca ttgttcacct 240  
 caccatactg cactcaggca agcaattctt tgctgggggg aactaatgac tctagctacc 300  
 tgggtgggtg ttaatttgga agatccagaa ttccgaggcg acgcgtctag agacctagta 360  
 gtcagttatg tcaacactaa tatgggccta aagttcaggc aactcttggt gtttcacatt 420  
 tcttgctcct cttttggaag agaaaccgtt atagagtatt tgggtgtctt cgagagtgtg 480  
 attcgactc ctccagctta tagaccacca aatgccctta tcctatcaac acttccggaa 540  
 actactgttg ttagacgacg aggcaggtcc cctagaagaa gaactccctc gcctcgaga 600  
 cgaaggctct aatcgccgct tcgcagaaga tctcaatctc gggaacctca atgttagtat 660

tcc

663

&lt;210&gt; 4

&lt;211&gt; 1047

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:

DNA coding for a fusion protein comprising a LHBs and  
heterologous binding site RGD

&lt;400&gt; 4

atggggccgtg gcgaaggagc tggagcattc gggctgggtt tcaccccacc gcaecggaggc	60
cttttggggt ggagccctca ggctcagggc atactacaaa ctttgccagc aaatccgcct	120
cctgcctcca ccaatcgcca gacaggaagg cagcctaccc cgctgtctcc acctttgaga	180
aacactcatc cttagggcat gcagtggaat tccacaacct ttcaccaaac tctgcaagat	240
cccagagtga gaggcctgta tttccctgct ggtggctcca gttcaggagc agtaaaccct	300
gttccgacta ctgcctctcc ctlatcgta atcttctcga ggattgggga cctgcgctg	360
aacatggaga acatcacatc aggatcccta ggaccccttc tcgtgttaca ggcgggggtt	420
ttcttgttga caagaatcct cacaataccg cagagtctag actcgtggtg gacttctctc	480
aattttctag ggggaactac cgtgtgtctt ggccaaaatt cgcagtcctc aacctccaat	540
cactcaccaa cctcctgtcc tccaacttgt cctggttatc gctggatgtg tctgcggcgt	600
tttatcatct tctcttcat cctgtctgta tgcctcatct tcttgttggg tcttctggac	660
tatcaaggta tgttgcccg tttgtctcta attccaggat cctcaaccac cagcagcggga	720
ccatgccgaa cctgcatgac tactgtctca ggaacctcta tgtatccctc ctgttctgtg	780
accaaaccct cgagcggaaa ttgcacctgt attcccatcc catcatcctg ggctttcgga	840
aaattcttat gggagtgggc cttagccctt ttctcctggc tcagtttact agtgccattt	900
gttcagtggg tcgtagggct ttccccact gtttggcttt cagttatatg gatgatgtgg	960
tattgggggc caagtctgta cagcatcttg agtccctttt taccgctgtt accaattttc	1020
ttttgtcttt ggtatacat ttaaacc	1047

&lt;210&gt; 5

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:

Primer

**THE UNIVERSITY OF CHICAGO**

35

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<220>
<223> Description of the artificial sequence:
        Primer
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33

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<220>
<223> Description of the artificial sequence:
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33

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<223> Description of the artificial sequence:
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<220>
<223> Description of the artificial sequence:
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<400> 9

aaaagatctg gccgtggcga aggagctgga gcattc

36

<210> 10

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:  
Primer

<400> 10

aaaagatctg gtttaaattgt atacccaaag

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<210> 11

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:  
Primer

<400> 11

cccgatatca tgtcatctct tgttcattgta cta

33

<210> 12

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:  
Primer

<400> 12

ggggatatcg gtcgatgtcc atgccccaaa

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<210> 13

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:  
Primer

<400> 13

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gggggatccc gatgtacggg ccagatatac gcgttg

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 <211> 27  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence:  
 Primer

<400> 14

gggggatccg cggcgcgttt acttgta

27

<210> 15  
 <211> 57  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence:  
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<400> 15

nnnagatcta tgcccatatc gtcaatcttc tcgaggattg gggaccctgg atccnnn

57

<210> 16  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence:  
 Primer

<400> 16

nnnggatcca ctgttcaagc ctccaagctg

30

<210> 17  
 <211> 36  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence:  
 Primer

<400> 17

nnngaattct ggatcttcca aattaacacc caccaca

36

20250909 14:00:00

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<220>
<223> Description of the artificial sequence:
        Primer
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nnngaattcc gaggcgacgc gtctagagac ctagtagtc

39

<220>  
<223> Description of the artificial sequence:  
Primer

nnnaagcttt cccacctta tgagtccaag

30